

RAW SEQUENCE LISTING

COPY OF PAPERS PATENT APPLICATION US/09/218,913D
ORIGINALLY FILED

1652

DATE: 02/05/2002
TIME: 04:40:07

INPUT SET: S36744770

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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FEB 12 2002
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SEQUENCE LISTING

1
2
3 (1) General Information:
4 (i) APPLICANT: Grace Maresh and Alan Snow
5 (ii) TITLE OF INVENTION: Therapeutic and Diagnostic Applications
6 of Perlecan Domain I Splice Variants
7 (iii) NUMBER OF SEQUENCES: 20
8 (iv) CORRESPONDENCE ADDRESS:
9 (A) ADDRESSEE: Patrick M. Dwyer
10 (B) STREET: 1818 Westlake Avenue N, Suite 114
11 (C) CITY: Seattle
12 (D) STATE: WA (Washington)
13 (E) COUNTRY: United States of America
14 (F) ZIP: 98109
15 (v) COMPUTER READABLE FORM:
16 (A) MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
17 (B) COMPUTER: IBM PC
18 (C) OPERATING SYSTEM: PC-DOS (Windows NT '95)
19 (D) SOFTWARE: WordPerfect 9
20 (vi) CURRENT APPLICATION DATA:
--> 21 (A) APPLICATION NUMBER:
22 (B) FILING DATE: 26-August-1997
--> 23 (C) CLASSIFICATION: Unknown
24 (vii) PRIOR APPLICATION DATA: n/a
25 (viii) ATTORNEY/AGENT INFORMATION:
26 (A) NAME: Dwyer, Patrick M.
27 (B) REGISTRATION NUMBER: 32,411
28 (C) REFERENCE/DOCKET NUMBER: PROTEO.P02
29 (ix) TELECOMMUNICATION INFORMATION:
30 (A) TELEPHONE: (206) 343-7074
31 (B) TELEFAX: (206) 343-7085
32
33
34 (2) INFORMATION FOR SEQ ID NO:1:
35
36 (i) SEQUENCE CHARACTERISTICS:
37 (A) LENGTH: 573 NUCLEOTIDES
38 (B) TYPE: NUCLEIC ACID
39 (C) STRANDEDNESS: SINGLE
40 (D) TOPOLOGY: LINEAR
41
42 (ii) MOLECULE TYPE: cDNA
43
44 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
45
46 ATGGGGTGGC GGGCGCCGGG CGCGCTGCTG CTGGCGCTGC TGCTGCACGG 50

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47 GCGGCTGCTG GCGGTGACCC ATGGGCTGAG GGCATACGAT GGCTTGTCTC 100
48 TGCCTGAGGA CACAGAGACC GTCACAGCAA GCCAAATGCG CTGGACACAT 150
49 TCGTACCTTT CTGATGATGA GGACATGCTG GCTGACAGCA TCTCAGGAGA 200
50 CGACCTGGGC AGTGGGGACC TGGGCAGCGG GGACTTCCAG ATGGTTTATT 250
51 TCCGAGCCCT GGTGAATTC ACTCGCTCCA TCGAGTACAG CCCTCAGCTG 300
52 GAGGATGCAG GCTCCAGAGA GTTTCGAGAG GTGTCCGAGG CTGTGGTAGA 350
53 CACGGGAGCT GGATGGCTGG GTTTTGTGG AGCTCGATGT GGGCTCCGAA 400
54 GGAATGCGG ATGGTGCTCA GATTCAGGAG ATGCTGCTCA GGGTCATCTC 450
55 CAGCGGCTCT GTGGCCTCCT ACGTCACCTC TCCCCAGGGA TTCCAGTTCC 500
56 GACGCCTGGG CACAGTGCCC CAGTTCCCAA GAGCCTGCAC GGAGGCCGAG 550
57 TTTGCCTGCC ACAGCTACAA TGA 573

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58

59

60

61 (2) INFORMATION FOR SEQ ID NO:2:

62

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 219 NUCLEOTIDES

65 (B) TYPE: NUCLEIC ACID

66 (C) STRANDEDNESS: SINGLE

67 (D) TOPOLOGY: LINEAR

68

69 (ii) MOLECULE TYPE: cDNA

70

71 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

72

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73 GGAGCT GGATGGCTGG GTTTTGTGG AGCTCGATGT GGGCTCCGAA 46
74 GGAATGCGG ATGGTGCTCA GATTCAGGAG ATGCTGCTCA GGGTCATCTC 96
75 CAGCGGCTCT GTGGCCTCCT ACGTCACCTC TCCCCAGGGA TTCCAGTTCC 146
76 GACGCCTGGG CACAGTGCCC CAGTTCCCAA GAGCCTGCAC GGAGGCCGAG 196
77 TTTGCCTGCC ACAGCTACAA TGA 219

```

78

79

80

81 (2) INFORMATION FOR SEQ ID NO:3:

82

83 (i) SEQUENCE CHARACTERISTICS:

84 (A) LENGTH: 190 AMINO ACIDS

85 (B) TYPE: AMINO ACID

86 (C) STRANDEDNESS:

87 (D) TOPOLOGY: LINEAR

88

89 (ii) MOLECULE TYPE: PROTEIN

90

91 (ix) FEATURE:

92 (D) OTHER INFORMATION: AMINO ACID NUMBERING ACCORDING TO
93 TRANSLATION OF GENBANK ACCESSION #M85289

94

95 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

96

97 Met Gly Trp Arg Ala Pro Gly Ala Leu Leu Leu Ala Leu Leu Leu

98 1 5 10 15

99 His Gly Arg Leu Leu Ala Val Thr His Gly Leu Arg Ala Tyr Asp

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100		20		25		30
101	Gly Leu Ser Leu	Pro Glu Asp Thr	Glu Thr Val Thr	Ala Ser Gln		
102		35		40		45
103	Met Arg Trp Thr	His Ser Tyr Leu	Ser Asp Asp Glu	Asp Met Leu		
104		50		55		60
105	Ala Asp Ser Ile	Ser Gly Asp Asp	Leu Gly Ser Gly	Asp Leu Gly		
106		65		70		75
107	Ser Gly Asp Phe	Gln Met Val Tyr	Phe Arg Ala Leu	Val Asn Phe		
108		80		85		90
109	Thr Arg Ser Ile	Glu Tyr Ser Pro	Gln Leu Glu Asp	Ala Gly Ser		
110		95		100		105
111	Arg Glu Phe Arg	Glu Val Ser Glu	Ala Val Val Asp	Thr Gly Ala		
112		110		115		120
113	Gly Trp Leu Gly	Phe Cys Gly Ala	Arg Cys Gly Leu	Arg Arg Glu		
114		125		130		135
115	Cys Gly Trp Cys	Ser Asp Ser Gly	Asp Ala Ala Gln	Gly His Leu		
116		140		145		150
117	Gln Arg Leu Cys	Gly Leu Leu Arg	His Leu Ser Pro	Gly Ile Pro		
118		155		160		165
119	Val Pro Thr Pro	Gly His Ser Ala	Pro Val Pro Lys	Ser Leu His		
120		170		175		180
121	Gly Gly Arg Val	Cys Leu Pro Gln	Leu Gln			
122		185		190		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

137	Gly Ala Gly Trp	Leu Gly Phe Cys	Gly Ala Arg Cys	Gly Leu Arg
138	1	5	10	15
139	Arg Glu Cys Gly	Trp Cys Ser Asp	Ser Gly Asp Ala	Ala Gln Gly
140		20	25	30
141	His Leu Gln Arg	Leu Cys Gly Leu	Leu Arg His Leu	Ser Pro Gly
142		35	40	45
143	Ile Pro Val Pro	Thr Pro Gly His	Ser Ala Pro Val	Pro Lys Ser
144		50	55	60
145	Leu His Gly Gly	Arg Val Cys Leu	Pro Gln Leu Gln	
146		65	70	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

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153 (A) LENGTH: 20 NUCLEOTIDES
154 (B) TYPE: NUCLEIC ACIDS
155 (C) STRANDEDNESS: SINGLE
156 (D) TOPOLOGY: LINEAR
157
158 (ii) MOLECULE TYPE: OLIGONUCLEOTIDE PRIMER
159
160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
161
162 CATCCAGCTC CCGTGTCTAC 20
163
164
165 (2) INFORMATION FOR SEQ ID NO:6:
166
167 (i) SEQUENCE CHARACTERISTICS:
168 (A) LENGTH: 312 NUCLEOTIDES
169 (B) TYPE: NUCLEIC ACIDS
170 (C) STRANDEDNESS: SINGLE
171 (D) TOPOLOGY: LINEAR
172
173 (ii) MOLECULE TYPE: cDNA
174
175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
176
177 ATGGGGTGGC GGGCGCCGGG CGCGCTGCTG CTGGCGCTGC TGCTGCACGG 50
178 GCGGCTGCTG GCGGTGACCC ATGGGCTGAG GGCATACGAT GGCTTGTCTC 100
179 TGCCTGAGGA CATAGAGACC GTCACAGCAA GCCARATGCG CTGGACACAT 150
180 TCGTACCTTT CTGATGATGA GGACATGCTG GCTGACAGCA TCTCAGGAGA 200
181 CGACCTGGGC AGTGGGGACC TGGGCAGCGG GGACTTCCAG ATGGTTTAAG 250
182 GAGATGCTGC TCAGGGTTCA TCTCCAGCGG CTCTGTGGCC TCCTACGTCA 300
183 CCTCTCCCA GG 312
184
185
186 (2) INFORMATION FOR SEQ ID NO:7:
187
188 (i) SEQUENCE CHARACTERISTICS:
189 (A) LENGTH: 82 AMINO ACIDS
190 (B) TYPE: AMINO ACID
191 (C) STRANDEDNESS:
192 (D) TOPOLOGY: LINEAR
193
194 (ii) MOLECULE TYPE: PROTEIN
195
196 (ix) FEATURE:
197 (D) OTHER INFORMATION: AMINO ACID NUMBERING ACCORDING TO
198 TRANSLATION OF GENBANK ACCESSION #M85289
199
200 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
201
202 Met Gly Trp Arg Ala Pro Gly Ala Leu Leu Leu Ala Leu Leu Leu
203 1 5 10 15
204 His Gly Arg Leu Leu Ala Val Thr His Gly Leu Arg Ala Tyr Asp
205 20 25 30

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206 Gly Leu Ser Leu Pro Glu Asp Ile Glu Thr Val Thr Ala Ser Gln
207 35 40 45
208 Met Arg Trp Thr His Ser Tyr Leu Ser Asp Asp Glu Asp Met Leu
209 50 55 60
210 Ala Asp Ser Ile Ser Gly Asp Asp Leu Gly Ser Gly Asp Leu Gly
211 65 70 75
212 Ser Gly Asp Phe Gln Met Val
213 80
214
215
216

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: OLIGONUCLEOTIDE PRIMER

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAGATGGTTT AAGGAGATGC TG 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 NUCLEOTIDES

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGCTCAGGGC AGCCCCTGGG CCGCCCGCCC GTG 33

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 AMINO ACIDS

(B) TYPE: AMINO ACID

(C) STRANDEDNESS:

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: